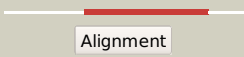
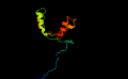
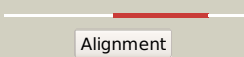
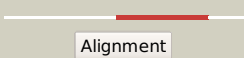
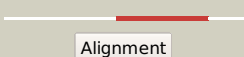
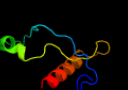
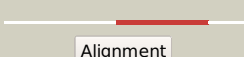
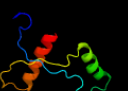
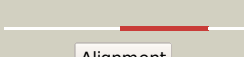
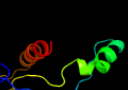


Phyre2

Email	member2smile@hotmail.com
Description	wolf_prion_protein
Date	Sat Dec 6 06:49:10 GMT 2014
Unique Job ID	e693307ba0c48822

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2lftA_	 Alignment		100.0	84	PDB header: membrane protein Chain: A: PDB Molecule: major prion protein; PDBTitle: human prion protein with e219k protective polymorphism
2	dli4ma_	 Alignment		100.0	87	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
3	d1xyqa_	 Alignment		100.0	94	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
4	d1xyxa_	 Alignment		100.0	93	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
5	d1xyua_	 Alignment		100.0	96	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
6	d1xyka_	 Alignment		100.0	99	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
7	d1u3ma_	 Alignment		100.0	47	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
8	d1tqba_	 Alignment		100.0	95	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
9	d1dwya_	 Alignment		100.0	92	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
10	c1dx0A_	 Alignment		100.0	92	PDB header: prion protein Chain: A: PDB Molecule: prion protein; PDBTitle: bovine prion protein residues 23-230
11	d1uw3a_	 Alignment		100.0	94	Fold: Prion-like Superfamily: Prion-like Family: Prion-like

12	c1fo7A_	Alignment		100.0	88	PDB header: membrane protein Chain: A: PDB Molecule: prion protein; PDBTitle: human prion protein mutant e200k fragment 90-231
13	d1fo7a_	Alignment		100.0	88	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
14	d1b10a_	Alignment		100.0	88	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
15	c1xu0A_	Alignment		100.0	39	PDB header: membrane protein Chain: A: PDB Molecule: prion protein; PDBTitle: solution structure of xenopus leavis prion protein
16	d1xu0a_	Alignment		100.0	39	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
17	d1u5la_	Alignment		100.0	51	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
18	c1skhA_	Alignment		99.7	83	PDB header: unknown function Chain: A: PDB Molecule: major prion protein 2; PDBTitle: n-terminal (1-30) of bovine prion protein
19	c2lbgA_	Alignment		99.2	93	PDB header: membrane protein Chain: A: PDB Molecule: major prion protein; PDBTitle: structure of the chr of the prion protein in dpc micelles
20	c1m25A_	Alignment		99.1	96	PDB header: unknown function Chain: A: PDB Molecule: major prion protein; PDBTitle: structure of synthetic 26-mer peptide containing 145-1692 sheep prion protein segment and c-terminal cysteine in tfe3 solution
21	c2iv5A_	Alignment	not modelled	96.4	88	PDB header: prion protein Chain: A: PDB Molecule: major prion protein; PDBTitle: hprp-173-195 solution structure
22	c2iv6A_	Alignment	not modelled	94.9	81	PDB header: prion protein Chain: A: PDB Molecule: major prion protein; PDBTitle: hprp-173-195-d178n solution structure
23	d1i17a_	Alignment	not modelled	91.9	33	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
24	d1lg4a_	Alignment	not modelled	81.2	31	Fold: Prion-like Superfamily: Prion-like Family: Prion-like
25	c2d2cH_	Alignment	not modelled	17.4	67	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit viii; PDBTitle: crystal structure of cytochrome b6f complex with dbmib from m.2 lammosus
26	c2d2cU_	Alignment	not modelled	17.4	67	PDB header: photosynthesis Chain: U: PDB Molecule: cytochrome b6-f complex subunit viii; PDBTitle: crystal structure of cytochrome b6f complex with dbmib from m.2 lammosus
27	c1vf5H_	Alignment	not modelled	16.2	67	PDB header: photosynthesis Chain: H: PDB Molecule: protein pet n; PDBTitle: crystal structure of cytochrome b6f complex from m.lammosus
28	d2e74h1	Alignment	not modelled	16.2	67	Fold: Single transmembrane helix Superfamily: PetN subunit of the cytochrome b6f complex Family: PetN subunit of the cytochrome b6f complex
29	c1vf5U_	Alignment	not modelled	16.2	67	PDB header: photosynthesis Chain: U: PDB Molecule: protein pet n;

29	c1v30_	Alignment	not modelled	10.2	67	PDBTitle: crystal structure of cytochrome b6f complex from m.laminosus
30	c4i7zH_	Alignment	not modelled	16.1	67	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: crystal structure of cytochrome b6f in dopg, with disordered rieske2 iron-sulfur protein soluble domain
31	c4pv1H_	Alignment	not modelled	16.1	67	PDB header: electron transport/inhibitor Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: cytochrome b6f structure from m. laminosus with the quinone analog2 inhibitor stigmatellin
32	c4h13H_	Alignment	not modelled	15.8	67	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: crystal structure of the cytochrome b6f complex from mastigocladus2 laminosus with tds
33	c2e76H_	Alignment	not modelled	15.8	67	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
34	c4h0IH_	Alignment	not modelled	15.8	67	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: cytochrome b6f complex crystal structure from mastigocladus laminosus2 with n-side inhibitor nqno
35	c2e74H_	Alignment	not modelled	15.8	67	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: crystal structure of the cytochrome b6f complex from m.laminosus
36	c2e75H_	Alignment	not modelled	15.8	67	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
37	c3hmjB_	Alignment	not modelled	14.1	27	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: saccharomyces cerevisiae fas type i
38	d1vf5c1	Alignment	not modelled	13.8	43	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
39	d1hcza1	Alignment	not modelled	13.5	45	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Cytochrome f, large domain Family: Cytochrome f, large domain
40	c2zt9H_	Alignment	not modelled	12.8	67	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120
41	c4ogqH_	Alignment	not modelled	12.8	67	PDB header: electron transport Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: internal lipid architecture of the hetero-oligomeric cytochrome b6f2 complex
42	c4h44H_	Alignment	not modelled	12.8	67	PDB header: photosynthesis Chain: H: PDB Molecule: cytochrome b6-f complex subunit 8; PDBTitle: 2.70 a cytochrome b6f complex structure from nostoc pcc 7120
43	d1b8wa_	Alignment	not modelled	11.5	32	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
44	c2vkzC_	Alignment	not modelled	10.6	28	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
45	d1ex4a1	Alignment	not modelled	10.4	67	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
46	d1c6vx_	Alignment	not modelled	9.0	67	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
47	c1c6vX_	Alignment	not modelled	9.0	67	PDB header: dna binding protein Chain: X: PDB Molecule: protein (siu89134); PDBTitle: siv integrase (catalytic domain + dna biding domain2 comprising residues 50-293) mutant with phe 185 replaced3 by his (f185h)
48	c2pffA_	Alignment	not modelled	8.8	28	PDB header: transferase Chain: A: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase
49	c2pffG_	Alignment	not modelled	8.8	28	PDB header: transferase Chain: G: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase
50	c2pffD_	Alignment	not modelled	8.8	28	PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structural insights of yeast fatty acid synthase
51	d2io8a1	Alignment	not modelled	8.7	33	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Glutathionylspermidine synthase substrate-binding domain-like
52	d1ihwa_	Alignment	not modelled	7.6	36	Fold: SH3-like barrel Superfamily: DNA-binding domain of retroviral integrase Family: DNA-binding domain of retroviral integrase
53	c2pq4B_	Alignment	not modelled	7.5	57	PDB header: chaperone/oxidoreductase Chain: B: PDB Molecule: periplasmic nitrate reductase precursor; PDBTitle: nmr solution structure of napd in complex with napa1-352 signal peptide
54	d2cnqa1	Alignment	not modelled	7.2	12	Fold: SAICAR synthase-like Superfamily: SAICAR synthase-like Family: SAICAR synthase
55	c2uv8C_	Alignment	not modelled	7.0	28	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha (fas2); PDBTitle: crystal structure of yeast fatty acid synthase with stalled2

						acyl carrier protein at 3.1 angstrom resolution
56	c2vxdA_	Alignment	not modelled	6.5	40	PDB header: nuclear protein Chain: A: PDB Molecule: nucleophosmin; PDBTitle: the structure of the c-terminal domain of nucleophosmin
57	c4r7qA_	Alignment	not modelled	6.4	30	PDB header: signaling protein Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: the structure of a sensor domain of a histidine kinase from vibrio2 cholerae o1 biovar eltor str. n16961
58	c2l7qA_	Alignment	not modelled	5.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein found in conjugate transposon; PDBTitle: solution nmr structure of conjugate transposon protein bvu_1572(27-2 141) from bacteroides vulgatus, northeast structural genomics3 consortium target bvr155
59	c2llhA_	Alignment	not modelled	5.9	40	PDB header: dna binding protein, chaperone Chain: A: PDB Molecule: nucleophosmin; PDBTitle: nmr structure of npm1_c70
60	c3lphD_	Alignment	not modelled	5.9	33	PDB header: viral protein Chain: D: PDB Molecule: protein rev; PDBTitle: crystal structure of the hiv-1 rev dimer
61	c4i6xA_	Alignment	not modelled	5.6	20	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide-isomerase a5; PDBTitle: crystal structure of non-catalytic domain of protein disulfide2 isomerase-related (pdir) protein
62	c2ml6A_	Alignment	not modelled	5.5	57	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of hypothetical protein zp_02069618.1 from bacteroides2 uniformis atcc 8492
63	c3t9nG_	Alignment	not modelled	5.5	17	PDB header: membrane protein Chain: G: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: crystal structure of a membrane protein